

[illegible]

FIGURE 2

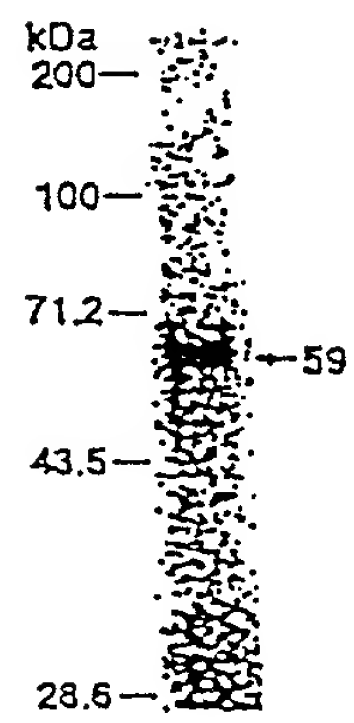


FIGURE 3

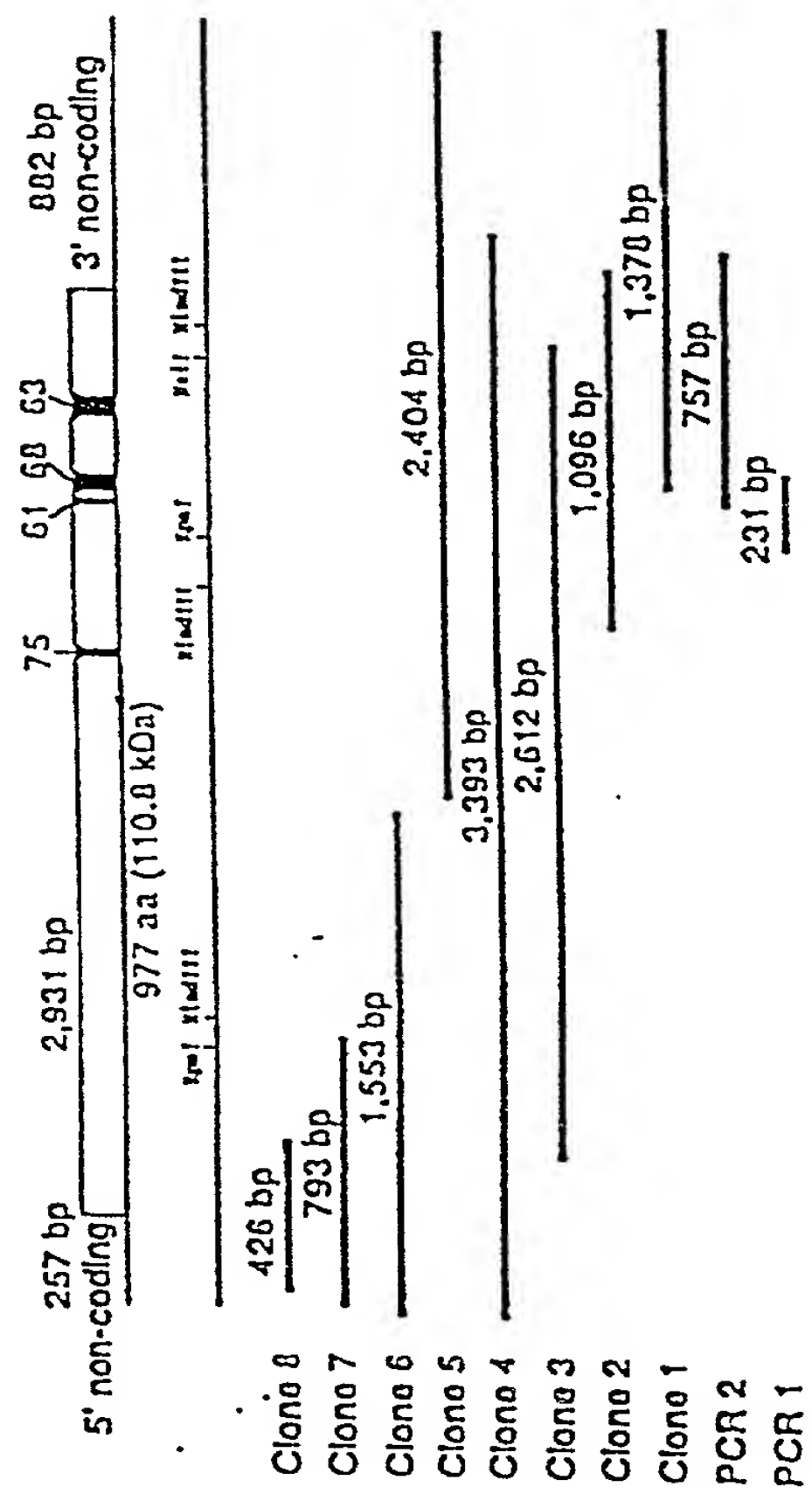


FIGURE 4

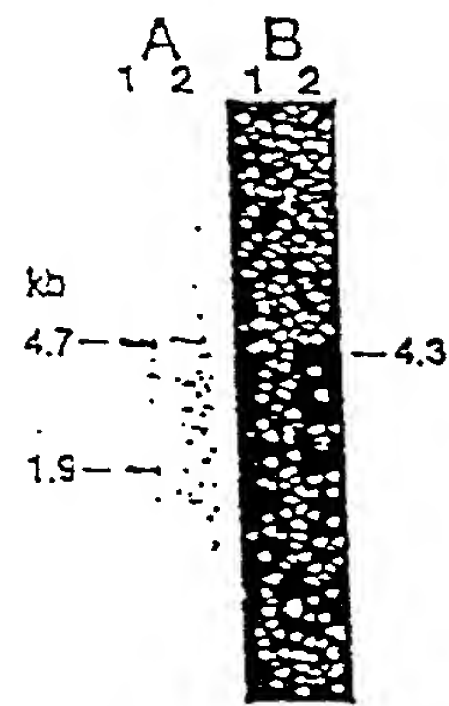


FIGURE 5

bPARC	(422)	ED.....	KRKEQCCEMKHQ RTE..	RKIPKYI PPH	SEQ ID NO: 19
hPARC	(421)	ED.....	RRKEQWETKHQ RTE..	RKIPKYV PPH	SEQ ID NO: 20
mPARC	(413)	ED.....	RRKEQCCEVRHQ RTE..	RKIPKYI PPN	SEQ ID NO: 21
CePARC	(29)	HQVPTMKRRKL	TEHGNTTESLLKEDP	PEEPS	SEQ ID NO: 22
hPARP	(205)	EG.....	KRKGD.EVDG.	VDEVAKKSKKEKDK	SEQ ID NO: 23
mPARP	(205)	EG.....	KRKGD.EVDG.	TDEVAKKSKRKETDK	SEQ ID NO: 24
bPARP	(208)	EG.....	KRKGD.EVDG.	IDEVTKKSKKEKDK	SEQ ID NO: 25
aPARP	(205)	EG.....	KRKGE.EVDG.	NVVAKKSKRKEKEK	SEQ ID NO: 26
XIPARP	(204)	EG.....	KRKAD.EVDG.	HSAATKKKIKKEKEK	SEQ ID NO: 27
DmPARP	(202)	EELPDTKRAKM.	ELSDTNEEGEKKQR.....		SEQ ID NO: 28
SpPARP	(205)	EGVSSAKKAKI.	EKIDEEAASIKELTEKIKK		SEQ ID NO: 29

FIGURE 6

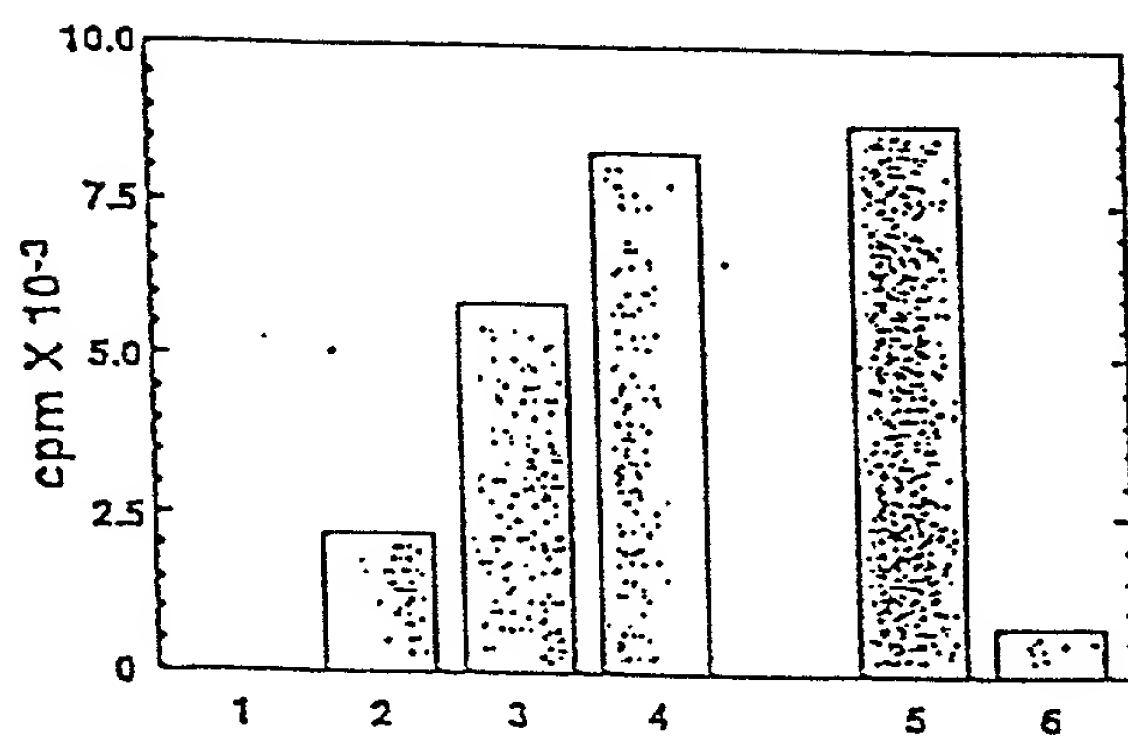


FIGURE 7

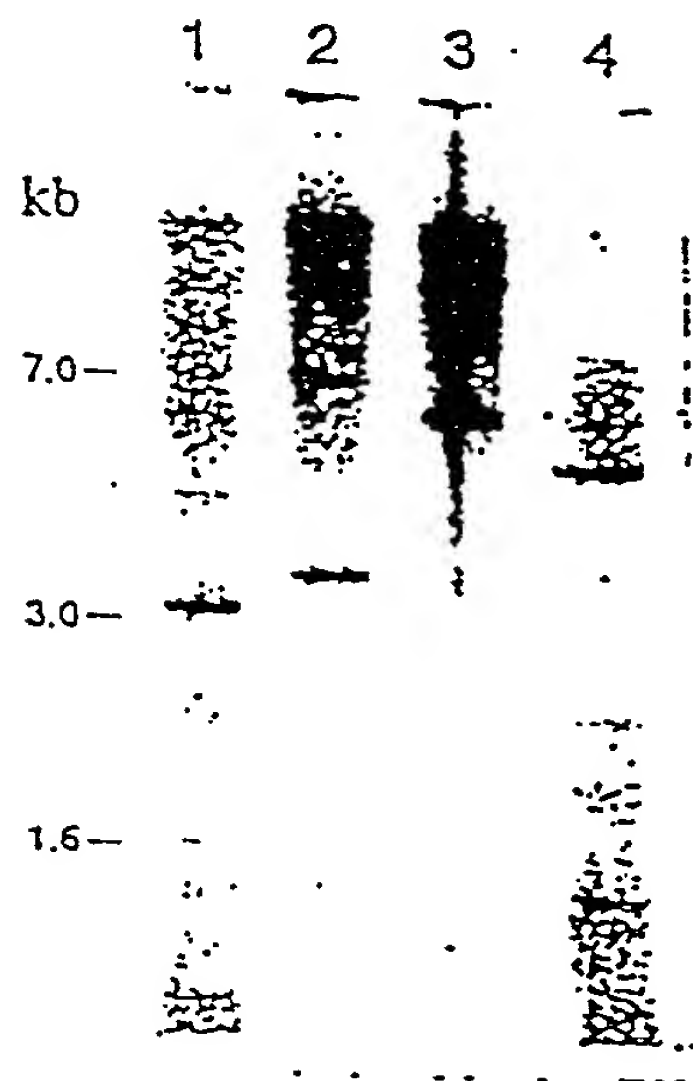


FIGURE 8

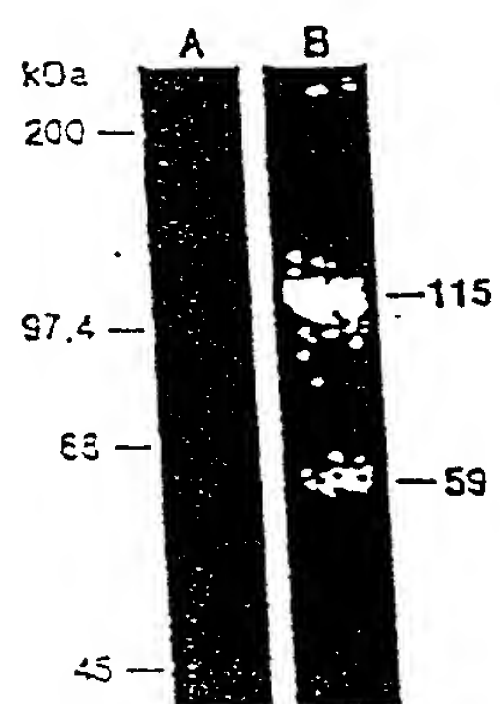


FIGURE 9

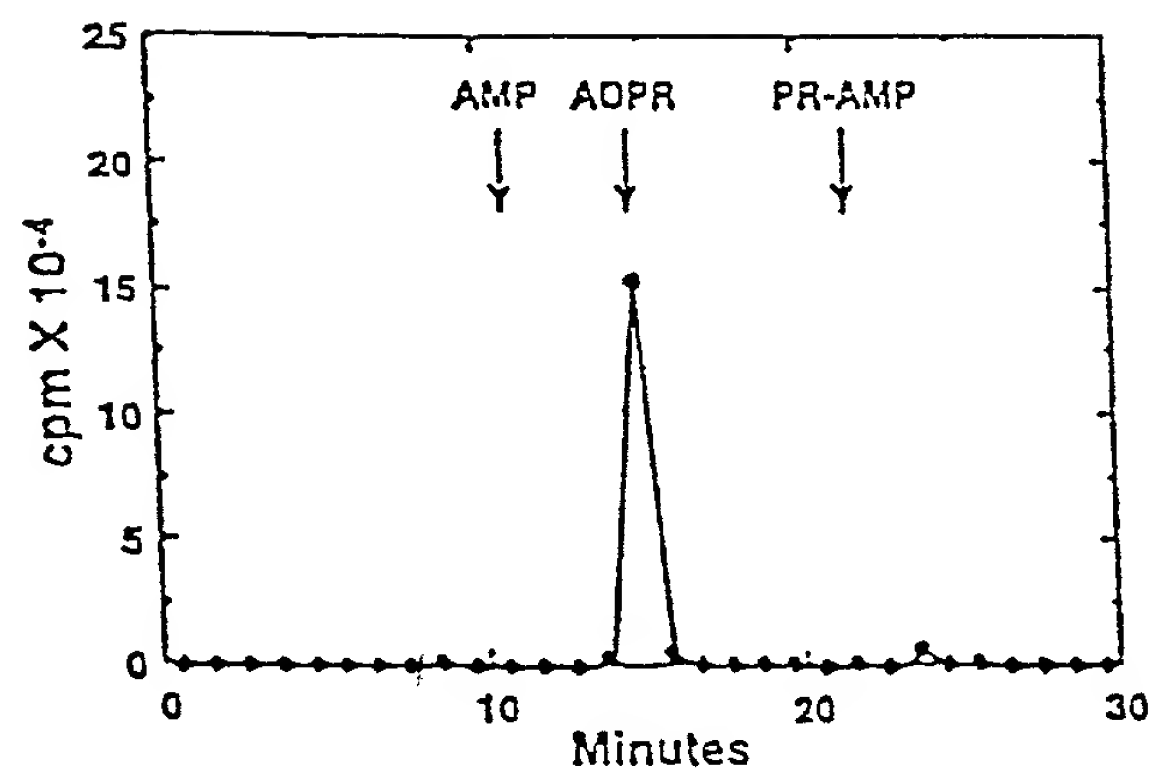


FIGURE 10

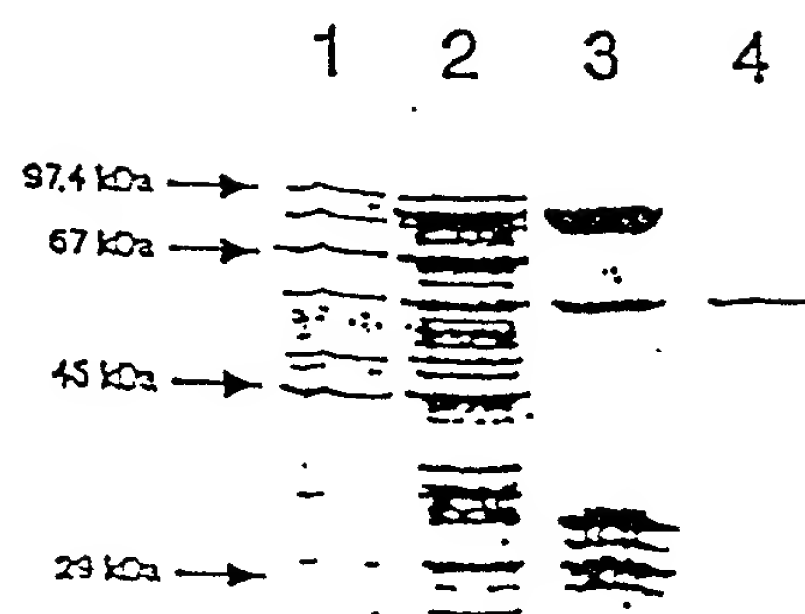


FIGURE 12

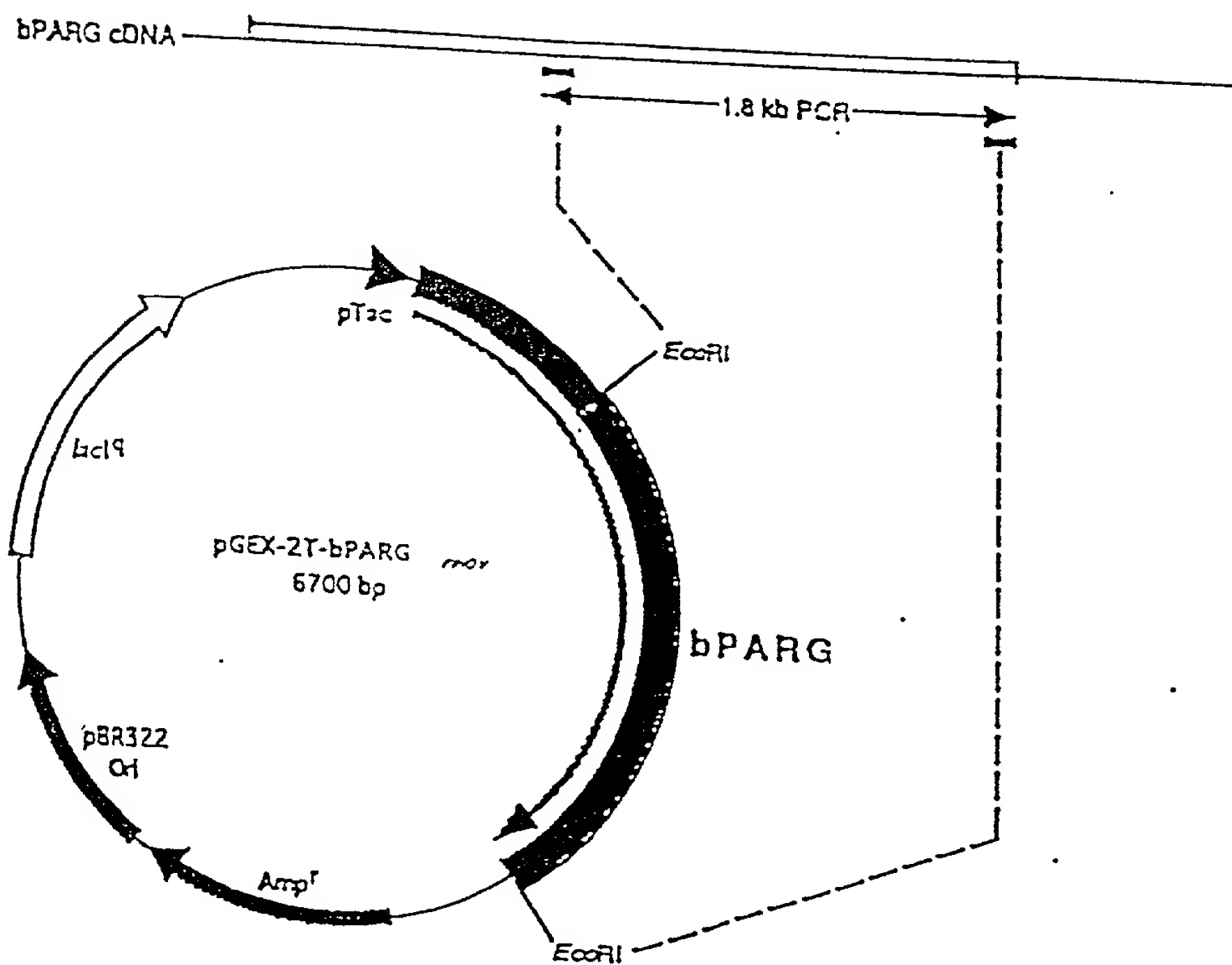


FIGURE 13

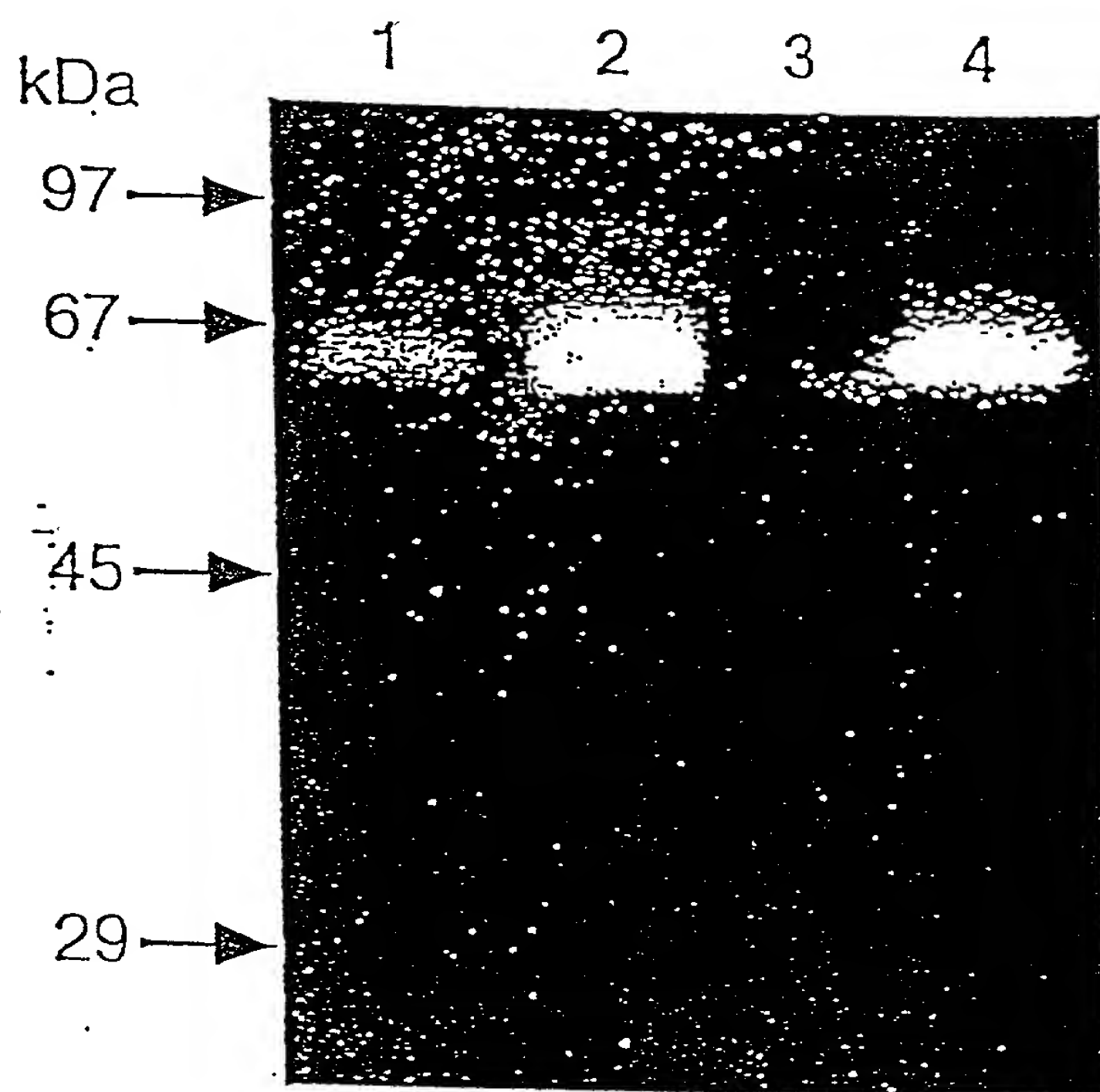
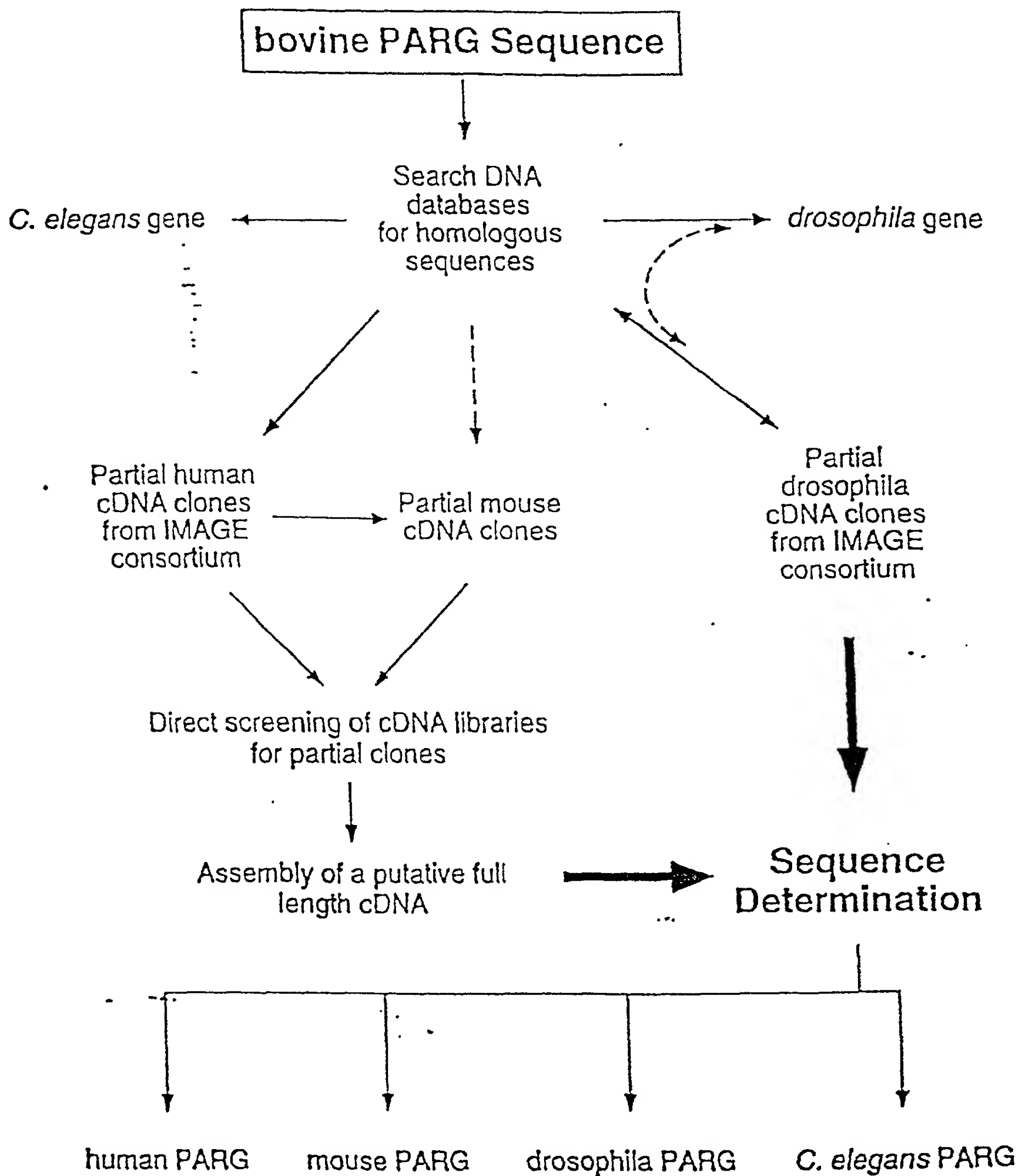


FIGURE 14

Strategy to Obtain Homologous PARG Sequences



Domain Organization of PARs

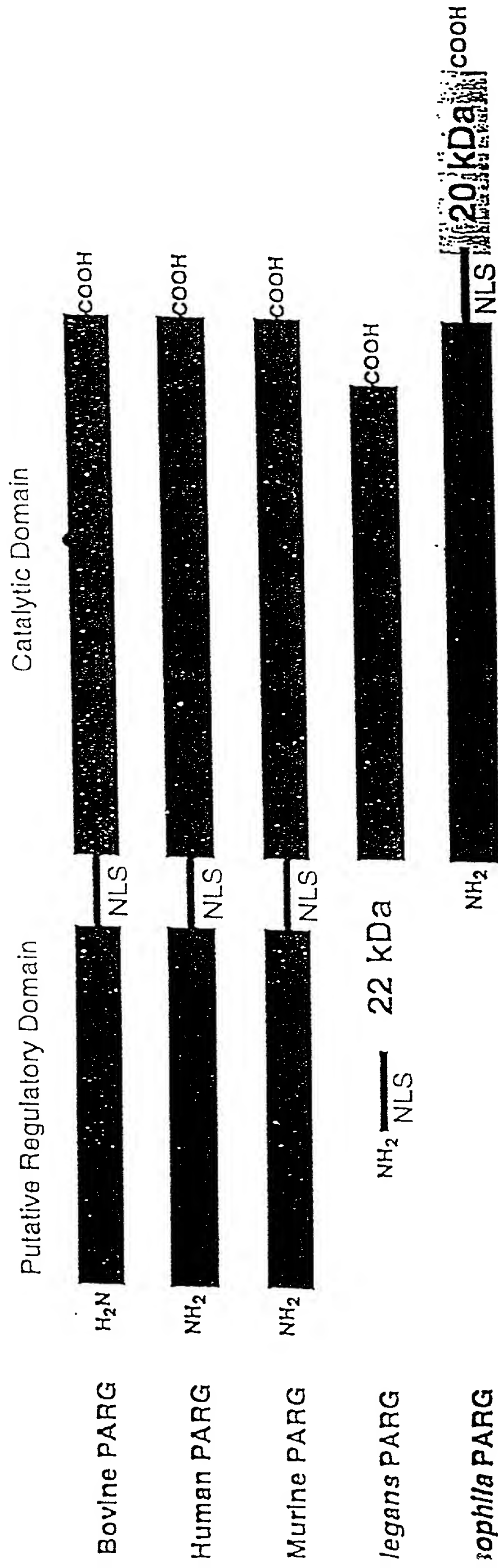


FIGURE 15

FIGURE 16

Multiple Alignment of Amino Acid Sequences of PARG from Different Species

```

Bparg 1 MSAGPGCEPCTKRPRWDAAATSPPAASDARSFPGRQRRVLDSDKAPVQFRVPPSSSGCALGRAGQHRGSATSLVFKQKTITSMWMDTKGIXTVESESLSBK
Hparg 1 MNAGPGCEPCTKATRWGAATTS.PAASDARSFPGRQRRVLDPKDAHVQFRVPPSSPACVPGQAGQHRGSATSLVFKQKTITSMWMDTKGIXTAESESLSBK
Mparg 1 MSAGPGCEPCTKA.RNGAAGTSAPTASDSRSFPGRQRRVLDPKDAHVQFRVPPSSPACVSGRAGPHERGNATSPVFKQKTITTWMDTKGPKTAESE...SK
Dparg 1 -----
Ceparg 1 -----

Bparg 101 EHNHTRREESMSSVQKDNFIQHNMEKLENVSQLGFDKSPVEKCTQYLKQHQTAAAMCKWQNEGPHSERLLESEPPAVTLVPEQFSAHVQDSSPKDDSDT
Hparg 100 EHNHTRIESMSSVQKDNFIQHNVEKLVNVSQSLDLKSLTEKSTQILNQHQTAAMCKWQNEGKHTEQLLESEPTVTLVPEQFSAHVQDSSPKDDSDT
Mparg 97 EHNHTRIDSMSVQKDNFIQHNVEKLENVSQLGFDKSPVEKCTQYLKQHQTAAAMCKWQNEGKHTEQLLESEPTVTLVPEQFSAHVQDSSPKDDSDT
Dparg 1 -----
Ceparg 1 -----MSKKFIELGDPVTQDEKDIYDY

Bparg 201 NSEESRDHQQFLTHVKL...ANAKQTMEDDEQGREARSHQKCGKACHPAEACAGCQQEETDVVSESPLSDTGSESDVGTGLKHAMRLNRQESSLGNSPFFEK
Hparg 200 DSEHRDMDQQFLTTVKL...ANAKQTMEDDEHAREAKSHQKCSKSGPGEDECASCQQDEIDVVPKSPLSDVGSESDVGTGSKNDKLRQESCLGNSPFFEK
Mparg 197 DHEEDRDHQQFLTPIKL...ANTKPTVGDGQ...ARSNCKCSCSRQSVKDCCTGCQQEEDVLPESPLSDVGABDGTGPKNDKLRQESSLGNSPFFEK
Dparg 1 -----
Ceparg 23 VGVGFABQVPTMKRRKLTEHGHTTESKEDPEEPKSRDVFVSSQSSDESQEDSAEMPEIAKEVSENCENLTETLKISHIESLDNVTERSEHTLDN....HK

Bparg 298 ESEPESPMDVDVNSKNSCQDSSEADEETSPGFDE.QEDSSSAQTANKPSRFQPREADTELKRKSSAKGGEIRLHPQFEGGESRAGMH.DVNAKRPGSTSSLN
Hparg 297 ESEPESPMDVDVNSKNSCQDSSEADEETSPGFDE.QEDGSSSAQTANKPSRFQARDADIEFRKRYSTKCGEVRLHPQFEGGESRTGMH.DLNAKLPGNISLN
Mparg 291 ESEPESPMDVDVNSKNSCQDSSEADEETSPVDFDE.QDDRSS.QTANKLSSCQAREADGDLRKRYLTGSEVRLHPQFE.GENNACTS.DLNAKPSGNSSLN
Dparg 1 -----
Ceparg 119 STEPHEE.DVNMKSHIDVAINSDDEDELVLLENKEMRDGEQVQQLS..QDLFADDQELIETPGIMKDTTTLQLOITDSEVETAQKMEMIESTEADSTFVG

Bparg 396 VECRNSKQHGRKDSKITDEPMRVPAKEDKRKEQCEMKHQRTERKIPKIIPPPLSPDKKWLGTPIEM..RMKPRCGIRLPPLRPSANHTVTIRVDLLRIG
Hparg 395 VECRNSKQHGRKDSKITDELMRLPKAEDRRKEQWETKHQRTERKIPKIIPPPLSPDKKWLGTPIEM..RMKPRCGIRLPPLRPSANHTVTIRVDLLRAG
Mparg 387 VECRNSKQHGRKDSKITDEPMRISKSEDRRKEQCEVRHQRTERKIPKIIPPPLSPDKKWLGTPIEM..RMKPRCGIRLPPLRPSASHTVTIRVDLLRAG
Dparg 32 .....THRLQK...ALCLHCARMSKSPDGCISEIE.....TREE.PENLANSL..DDSWRGVSMHAIRNRQPFELNLPVVTAGNLRHVMIQLFIRET.
Ceparg 216 EDSKATKTVRTSSSSP...LSTVSTCEAPAKGRARMIYQKELEKHVIAFTEGHLT.....LQPDNLKVDPDFRNIYI.CTIFNFPASQG...KLRED.WRIG

Bparg 494 EVPK.PPPTHYKDLWDNKEVKMPCSEQMLYPVEDENGE.RAAGSRWELIQTALLNRLTRPQNLKDAILKYNVAYSKKWDF TALIDFWDXVLEBAEAQHLY
Hparg 493 EVPK.PPPTHYKDLWDNKEVKMPCSEQMLYPVEDENGE.RTAGSRWELIQTALLNKFTRPQNLKDAILKYNVAYSKKWDF TALIDFWDXVLEBAEAQHLY
Mparg 485 EVPK.PPPTHYKDLWDNKEVKMPCSEQMLYPVEDENGE.RTAGSRWELIQTALLNKFTRPQNLKDAILKYNVAYSKKWDF TALIDFWDXVLEBAEAQHLY
Dparg 115 .PPR.PIKSPGK..NDSEHVRPCAPESKYPREXPDGS.TTIDFRMEMIERALLQPIKTCEELQAAIISYNTTYRDQWEPALHQLLDEELDESETRVFF
Ceparg 303 ..PKIVLPQRWRE.FDSRGRR...RDSIFYFKRLDQILKCYKTTGTFMFVGLLE.....NMWE..FDPDITIK....LPAL.EMHYKMSSELVGREEV

Bparg 592 QSIPLDMVKIALCLPHICTQPIPLLKQKMNHSITMSQEQIASLLANAFCTFPRRNA.KMKSEYISSYPDINFHRLFEGRSSRKPEKLKTLFCYFRRV..T
Hparg 591 QSIPLDMVKIALCLPHICTQPIPLLKQKMNHSITMSQEQIASLLANAFCTFPRRNA.KMKSEYISSYPDINFHRLFEGRSSRKPEKLKTLFCYFRRV..T
Mparg 583 QSIPLDMVKIALCLPHICTQPIPLLKQKMNHSITMSQEQIASLLANAFCTFPRRNA.KMKSEYISSYPDINFHRLFEGRSSRKPEKLKTLFCYFRRV..T
Dparg 210 EDLLPRIIRLALRLPDLIQSPVPLLKHEHNASLSLSQQQISCLLANAFCTFPRRNTLKRKSEYSTFPDINFHRLYQSTGPAVLEKLKXIMHYFRRVCPT
Ceparg 384 LEKPARVARIAKTAEDILPZRIYRLVGDVE.BATLSEKQCAALVARMFFA.....RPDSPPS.....FCRILSSDKSICVEKLKFLFTIF.....

Bparg 689 EKK....PTGLVTFTRQS.L.ED.F.PEWERCEKLL..TRLEVTIEGTIEGNGQGLQVDFANRFVGGGVTSAGLVQEEIRFLINPELIVSRLFTFVLDH
Hparg 688 EKK....PTGLVTFTRQS.L.ED.F.PEWERCEKPL..TRLEVTIEGTIEGNGQGLQVDFANRFVGGGVTSAGLVQEEIRFLINPELIVSRLFTFVLDH
Mparg 680 EKK....PTGLVTFTRQS.L.ED.F.PEWERCEKPL..TRLEVTIEGTIEGNGQGLQVDFANRFVGGGVTSAGLVQEEIRFLINPELIVSRLFTFVLDH
Dparg 310 ERDASNVTGVTFTVRRSGLPEH.L.IDMSQSAAPLGDVPLHVDAGETIEDEGIGLLQVDFANKYLGGGVLGHCVCVQEEIRFVICPELLVGLKLTTECLRP
Ceparg 463 DKMSMDPPDGAVSF.RLTMDKDTFNEEM.KDKKLRSLPEVEFFDEMLIEDTAL.CTQVDFANEHLGGGVLEHGSVQEEIRFLMCPKMHVGMLLCEKMKQ

Bparg 779 NECLIIITGTEQISEYTGIAETIRWA.....RSHEDRSE.RDDWQRRTTEIVAIDALHFR.RYLD....QFVPEKIRRELHKAICGFLRPGVSSENLSAVA
Hparg 778 NECLIIITGTEQISEYTGIAETIRWS.....RSHEDGSE.RDDCERRCTEIVAIDALHFR.RYLD....QFVPEKMRRELHKAICGFLRPGVSSENLSAVA
Mparg 770 NECLIIITGTEQISEYTGIAETIRWA.....RSHEDGSE.KDDWQRRTTEIVAIDALHFR.RYLD....QFVPEKVRRELHKAICGFLRPGVPSENLSAVA
Dparg 408 FEALVHLGAERISNYITGIAGSFENS.....GNFEDSTP.RDSSGRRTAIVAIDALHFA.QSHH....QYREDLMERELHKAIGFVHVMTTPP..PGVA
Ceparg 560 LEAISIVGAIYVSSITGIGETLEKNAELQPNHSRQNTNEFRDRFGRLRVETIAIDAILFKGSKLDCQTEQLNKANIIREMKKASIGFMSQGPFTNIP.IV

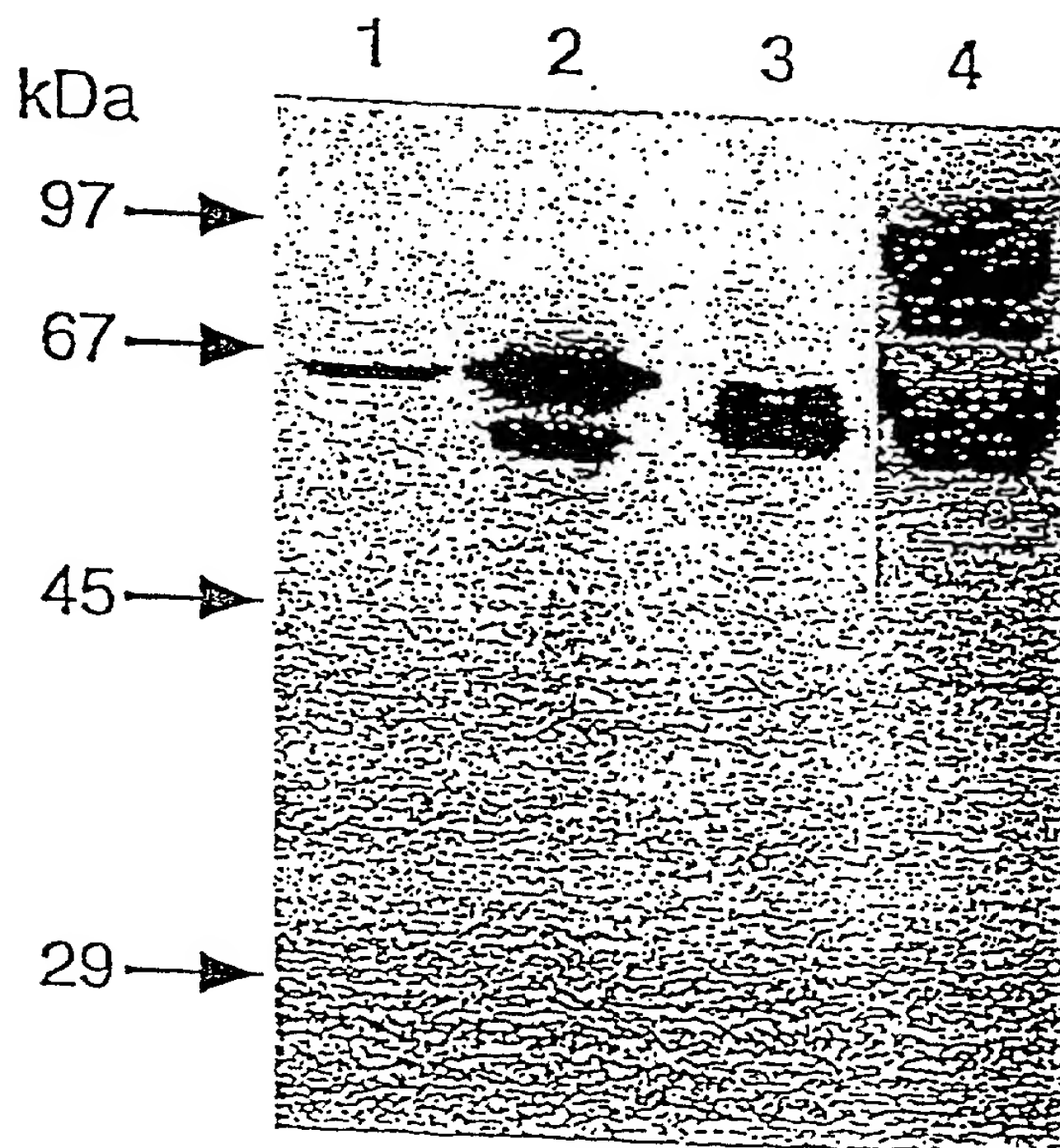
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Hparg 867 TGNWCCGAFGGDARLKALIQILAAAAAERDVVYFTFGDSELMRDIYSMHFTLTERKLTVGH.VIKLLLRYYNEECRNCSTPGP.....DIXLYPFIYHA
Mparg 859 TGNWCCGAFGGDARLKALIQILAAAAAERDVVYFTFGDSELMRDIYSMHFTLTERKLDVOK.VIKLLLRYYNEECRNCSTPGP.....DIXLYPFIYHA
Dparg 495 TGNWCCGAFGGDSILKALLQLHVCALGRPLAYYTFGNHVEFRDDFHEMWLLFRNDGTTVQQ.LWS.ILRYSRLIKEKSSKEPREMKASKKKLYDFI...
Ceparg 659 TGNWCCGAFNGDKPLKFIIQVIAAGVADRPLHFCBFGPELAACKKKIIRMKQKDVTLGKSCFSIFS-----

Bparg 961 VESCTQTTNQPGQRTGA-----
Hparg 960 VESCAETADESGQRTGT-----
Mparg 952 VESSAETTDMPGQKACT-----
Dparg 590 KEELKKVRDVPGEASAZAGSSRVAGLGEGKSEZTSKSSPELNKQPARPQITITQOSTDLLPAQLSQDNSNSSSEDQALLHLSDDDEANAHMEASLEAKS
Ceparg 727 -----

Bparg 978 -----
Hparg 977 -----
Mparg 969 -----
Dparg 690 SVEISNSSTTSKTSSTATKSHGSGGRQLSLLHLDTHYEKGSASKRPRKSPNCSKAEGSAKSRKEIDVTDKDEKDDIVD
Ceparg 727 -----

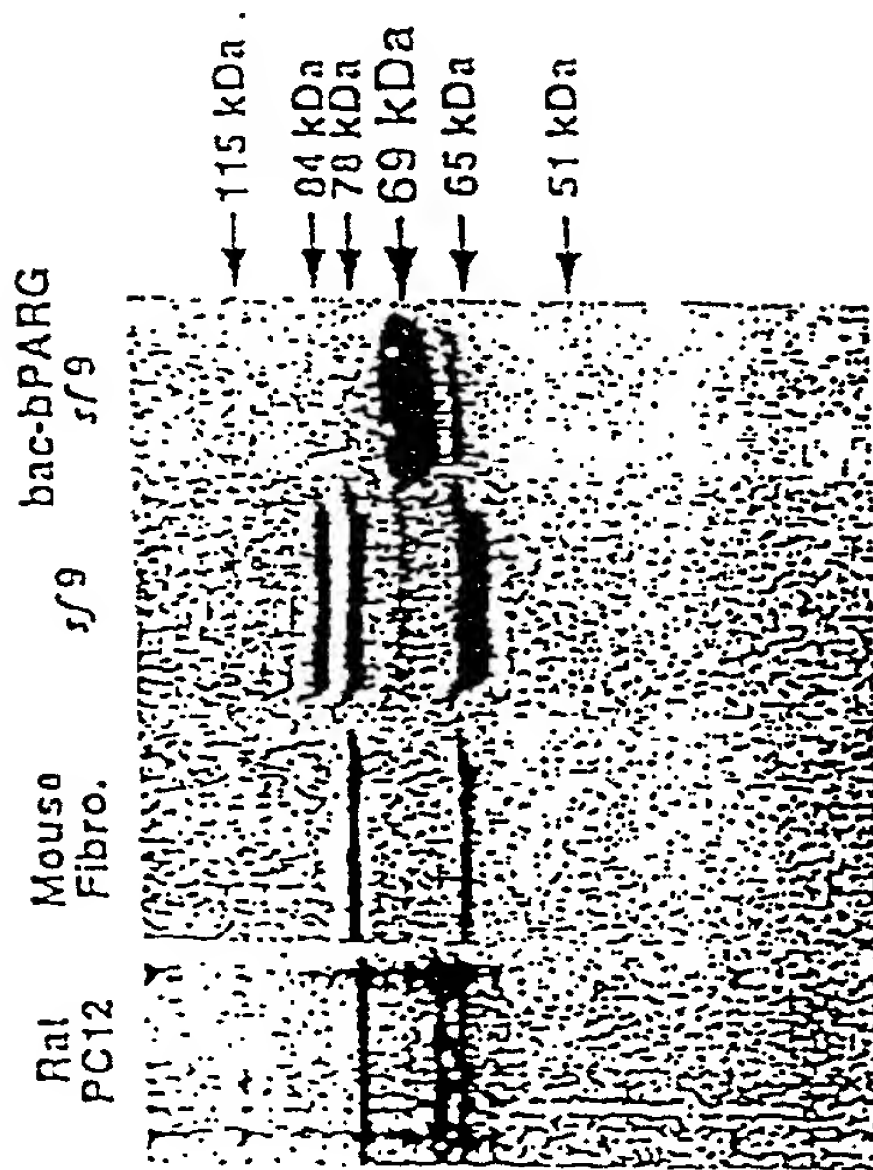
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FIGURE 17



B

Cell Extracts



A

Bovine Tissue

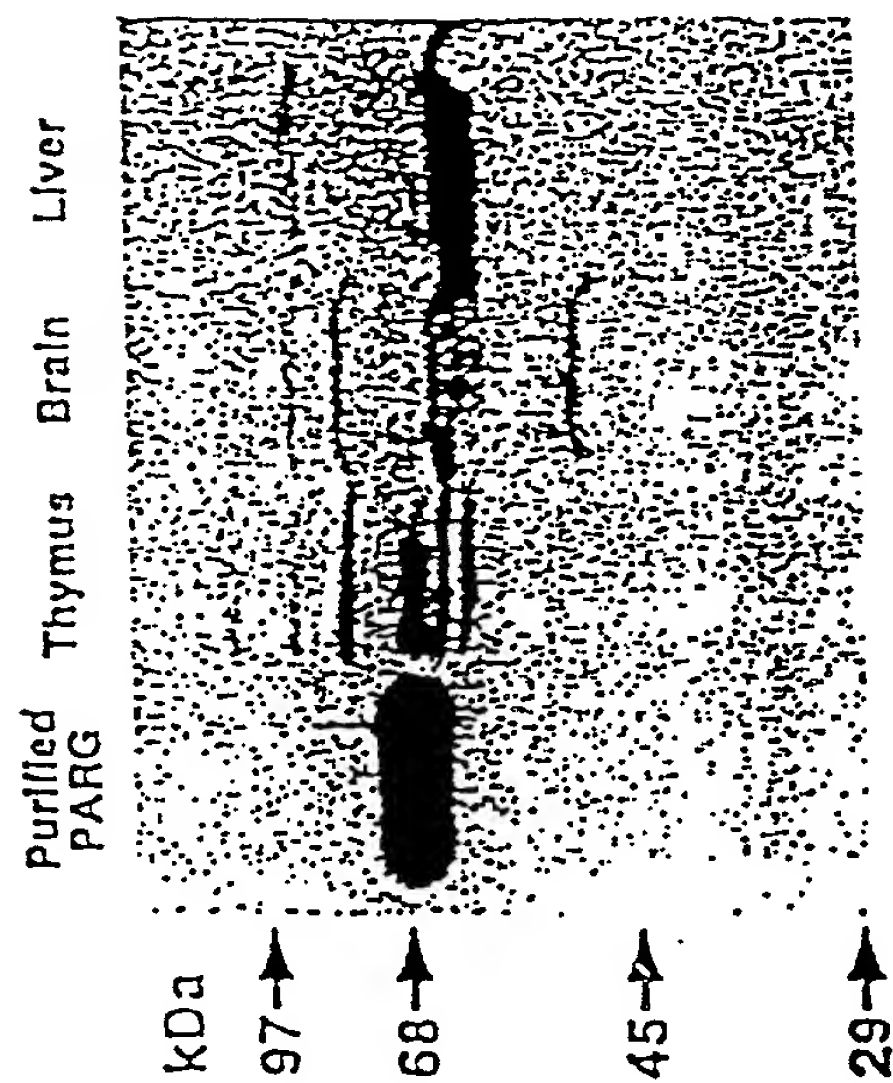


FIGURE 18

FIGURE 19

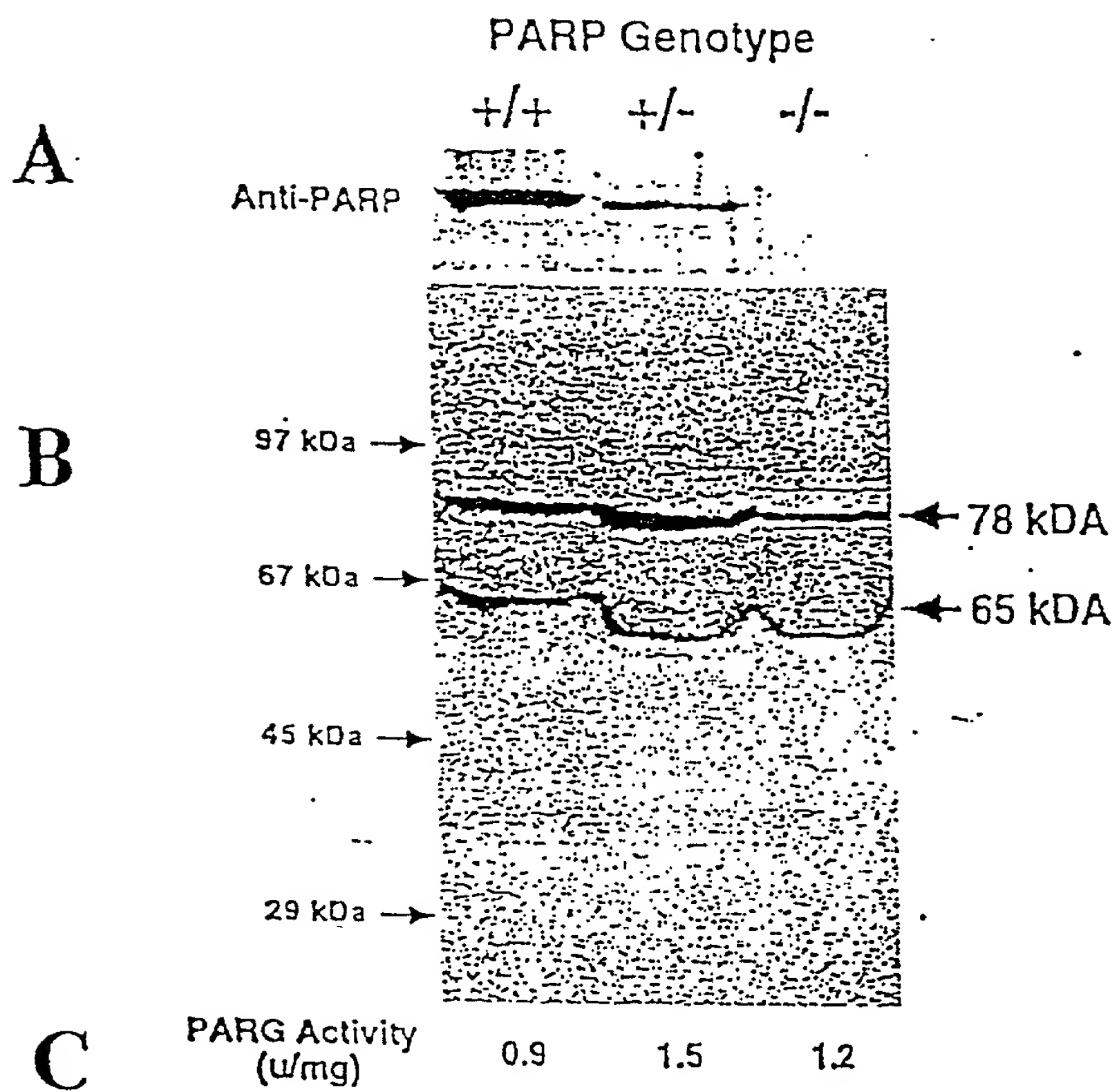


FIGURE 20

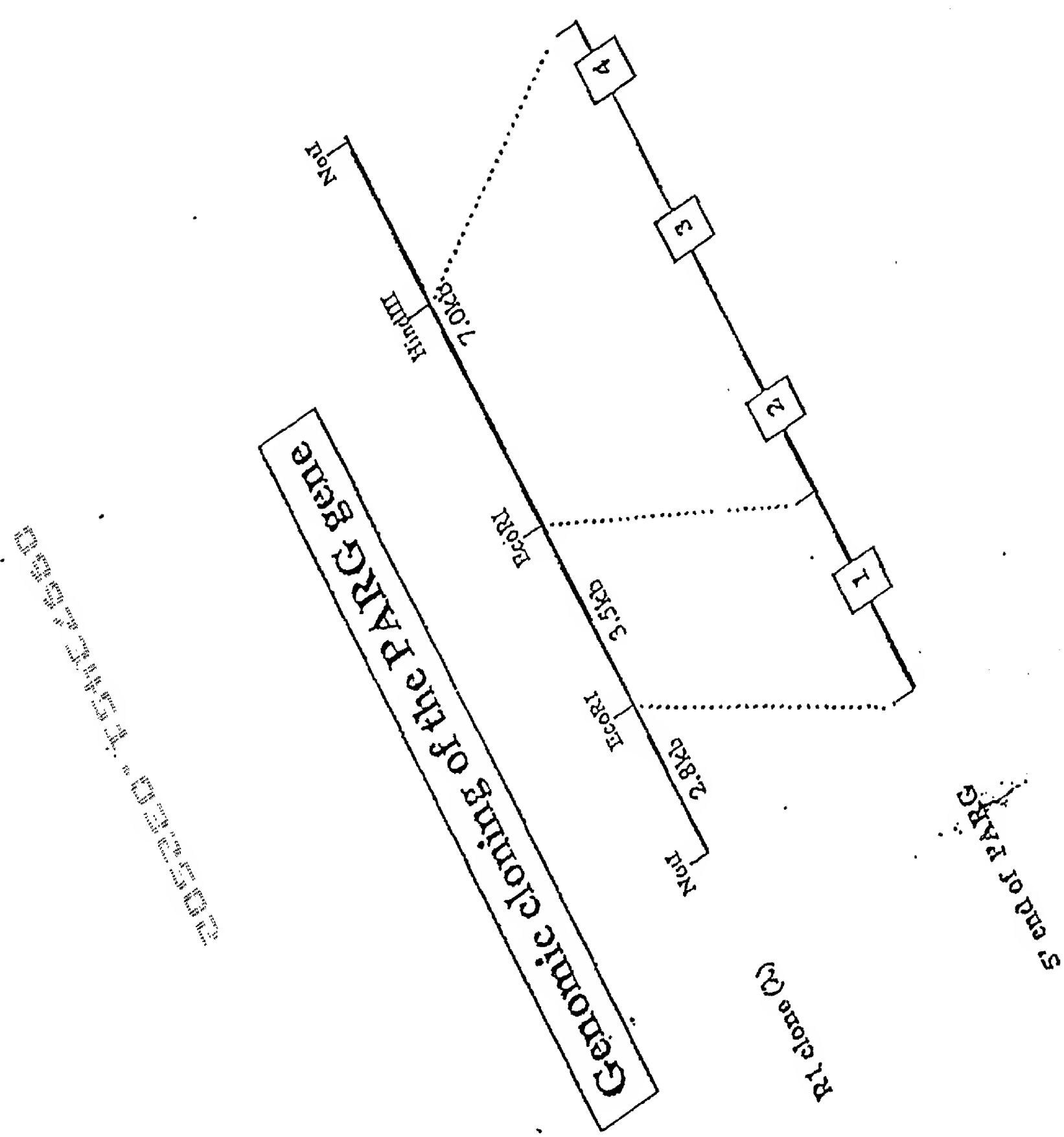


FIGURE 21

